Particle physics

# ‘Baryon junction’ gives proton its identity

José Guilherme Milhano & Néstor Armesto

A conserved property of protons and neutrons is carried not by their constituent particles but by structures that mediate the force between them.

The visible Universe owes its existence to the brief moments after the Big Bang when many of the laws of physics that hold the current Universe together were broken, allowing an imbalance between visible matter and antimatter to emerge[1]. One of these laws is the conservation of a quantity called baryon number, which is assigned to all protons and neutrons. Protons and neutrons are a type of particle called a baryon, which is made up of three fundamental particles known as quarks. Writing in *Science*, the STAR Collaboration[2] reports the strongest experimental evidence yet that baryon number is carried not by the quarks themselves but by structures called baryon junctions, which bind them together.

In the conventional interpretation, a baryon number of one-third is assigned to each of the three quarks — called valence quarks — that make up a baryon. This intuitive picture has, however, never been conclusively verified experimentally.

As well as the electromagnetic force, quarks interact through a force called the strong force, which is mediated through the exchange of particles known as gluons. This interaction is described by a theory called Quantum Chromodynamics (QCD), which was developed in the 1970s. Shortly after the introduction of QCD, an alternative theory was proposed by French physicist Xavier Artru[3] and by Italian physicists Giancarlo Rossi and Gabriele Veneziano[4]. In a baryon, the gluons form a Y-shaped structure called a baryon junction; in the alternative view, baryon number is carried not by the quarks but by this junction.

The junction’s three gluonic strings terminate on the valence quarks, so stating whether baryon number is lodged in the quarks or in the junction might initially seem to be a matter of convention. For most observable processes, the two scenarios are effectively indistinguishable. However, when atomic nuclei collide at high energies, theory predicts that this is no longer the case.

To settle the question of baryon-number transport (what is carrying the baryon number), the STAR Collaboration used results from the Relativistic Heavy Ion Collider (RHIC) at Brookhaven National Laboratory in Upton, New York (Fig. 1). The RHIC accelerates two beams of ions and collides them at relativistic speed (close to the speed of light). At such speeds, the time taken for an event to occur depends on the reference frame (viewpoint) of the observer, which depends on the observer’s velocity.

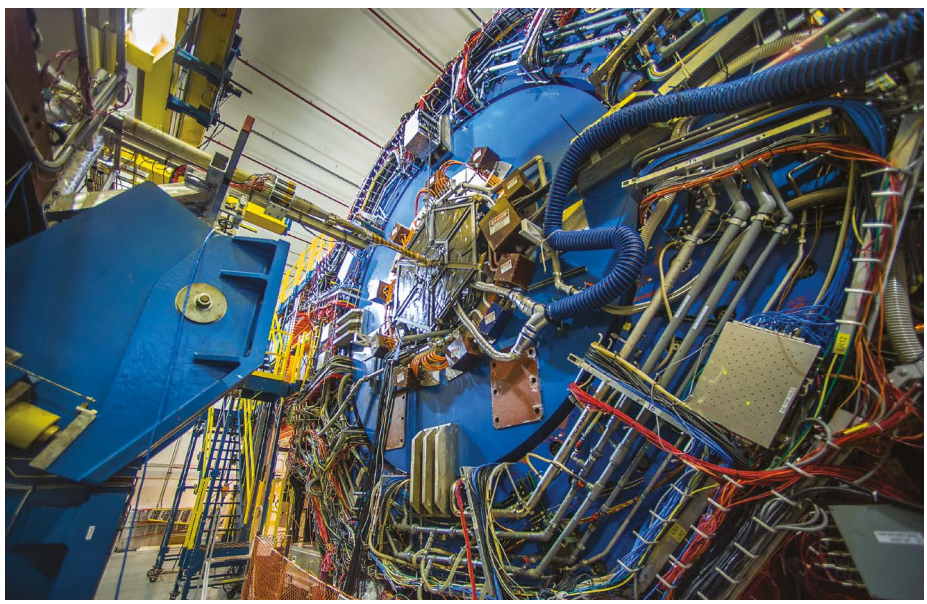
Rather than velocity, it is often more convenient to describe the particles involved in relativistic collisions using a quantity called rapidity, because it can be converted between reference frames more easily. In particle-physics experiments, rapidity is generally defined relative to the particle beam: if an object’s rapidity is zero, which is called mid-rapidity, the particle’s motion is entirely perpendicular to the beam; if the rapidity is much larger than zero, its motion is largely parallel to the beam.

Measurements of baryon number as a function of rapidity can differentiate the quark and baryon-junction transport scenarios. Before the collision, a nucleus’s baryon number is concentrated at rapidity far from zero, which is called forward rapidity. When a nucleus experiences a collision at relativistic speed, baryons are sometimes scattered into the mid-rapidity region.

The transport of baryon number from forward to mid-rapidity indicates that whatever carries the baryon number has undergone a large change in momentum. Quarks, being heavy and fast, are hard to drag from forward to mid-rapidity as a coordinated triplet, whereas baryon junctions, which are composed of gluons with lower momentum than quarks have, can be deflected much more easily[5].

The STAR collaboration interrogated these two theories using three separate measurements. First, it studied the collision between a photon and the nucleus of a gold atom. This is a particularly clean probe of baryon-number transport because a photon carries no baryon number. The authors found that the net-proton yield — a proxy for transported baryon number — falls off exponentially as rapidity gets closer to zero. This is consistent with the predictions of junction-mediated transport, and in disagreement with those of standard quark transport models.

Second, the authors examined previously published data on collisions between gold nuclei and showed that the shape of the fall-off in proton yield as rapidity decreases does not depend on whether the collisions between the gold-ion beams are glancing or head-on. This also contradicts the valence quark interpretation, which predicts that in the head-on-collision scenario, in which more protons and neutrons participate in collisions, a higher fraction of the total baryon number should be transported to mid-rapidity than is



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**Figure 1 | The STAR detector.** The STAR detector is an experiment at the Relativistic Heavy Ion Collider at Brookhaven National Laboratory in Upton, New York. It studies the products of high-energy ion–ion collisions.

the case in the glancing collision.

The third and, in our view, most striking result compares the transport of baryon number with that of electric charge. Quarks carry electric charge, but baryon junctions do not, so the ratio of baryon number to charge arriving at mid-rapidity offers a direct clue as to the identity of the carrier. To investigate this, the STAR collaboration performed two sets of collision experiments between two beams of either ruthenium-96 or zirconium-96 isotopes. These isotopes have the same total number of protons and neutrons altogether and therefore roughly the same mass, but different numbers of protons and therefore different charges. If valence quarks carry the baryon number, the electrical charge and baryon number should be transported together in a one-to-one ratio in all the collisions. Instead, in most head-on collisions, STAR measured a ratio nearly twice that of the valence-quark prediction.

Taken together, these three measurements converge on a picture in which an electrically neutral object, something that is influenced by the strong force but not electromagnetism, is the main vehicle for baryon-number transport. The baryon junction is currently the only candidate that accommodates all the observations.

The implications of this result reach beyond a technicality in QCD bookkeeping. If baryon number is bound to baryon junctions rather than to quarks, it alters how theorists should model the early Universe, when baryons emerged from a high-energy plasma of quarks and gluons. It could also aid the understanding of the structure of 'exotic' multi-quark particles, as well as hypothetical states made entirely from gluons that have yet to be observed. Because baryon number is an emergent property of the strong interaction, the finding that it defies simple quark-level explanation could point to unknown properties of QCD.

Further tests are needed, and future experiments are well-placed to provide them. The Electron–Ion Collider, under construction at Brookhaven National Laboratory, will probe the spatial distribution of baryon number inside protons and neutrons with unprecedented resolution, while ongoing programmes at the Large Hadron Collider at CERN, Europe's particle-physics laboratory near Geneva, Switzerland, and the Thomas Jefferson National Accelerator Facility in Newport News, Virginia, offer other perspectives. For now, we think that the STAR result marks a turning point. After 50 years of work, it seems that one of the proton's most fundamental properties resides not in its quarks, but in the gluonic web that binds them together.

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Developmental biology

# DNA-editing 'pencils' used in human embryos

**Sherif Khodeer & Vincent Pasque**

A genome-rewriting approach known as adenine base editing offers a precise way to investigate gene function in early human embryos. **See p.1281 & p.1289**

Writing in *Nature*, Bower *et al.*[1] (page 1281) and Jerabek *et al.*[2] (page 1289) describe how they have used a precision genome-editing tool, known as base editing, in human embryos to reveal how a key gene contributes to early development, and how embryos respond to specific DNA changes. The work sharpens scientists' view of this developmental stage while inevitably reactivating debates about heritable DNA editing.

Much of what we know about early mammalian development comes from studies of mouse embryos, but human embryos do not always follow the same rules. Direct studies in human embryos are therefore essential for reproductive medicine and for understanding genetic diseases. Many inherited conditions can be traced back to a change of a single DNA base, making precision-editing tools especially valuable for investigating how such mutations can affect development[3,4]. To study these changes in human embryos, scientists need genome-editing tools that can modify DNA precisely and with minimal unintended damage[5,6].

Conventional CRISPR–Cas9 editing works like molecular scissors, cutting both strands of a DNA double helix at a precise location. The goal is either to inactivate the gene at that location or to introduce a specific DNA change with the help of a repair template (a short piece of DNA carrying the intended sequence, which the cell can copy during the repair process). In human embryos, however, this repair is often unreliable, sometimes causing large DNA losses, structural chromosome damage or mosaicism — in which a mixture of cells have different editing outcomes[7]. This limits scientists' ability to interpret experimental results.

In base editing, by contrast, an enzyme that modifies DNA (such as a deaminase) is fused to a Cas9 'nickase' enzyme, allowing one DNA base to be converted into another without causing a double-strand break — acting more like a pencil than scissors[8]. By avoiding a large break, base editing offers a way to interrogate gene function while reducing the risk of unintended genomic damage. Bower and colleagues[1] now use base editing to uncover the role of a gene called *NANOG* in early human embryos. Jerabek *et al.*[2] assess the efficiency and genomic safety of base editing *PCSK9* — a gene involved in cholesterol metabolism and linked to heart-disease risk.

Bower *et al.*[1] first validated their strategy in human embryonic stem cells, using a base editor that targets adenine bases to disrupt *NANOG*. The edited stem cells lost the molecular signatures of pluripotency (the ability to self-renew and to generate nearly all cell types of the body) and could no longer maintain themselves as stem cells. Therefore, the authors determined that *NANOG* is required to preserve human pluripotency.

The team then applied the same strategy to human embryos. Disrupting *NANOG* did not prevent the formation of the early hollow ball of cells known as the blastocyst, but it did reduce the quality of the blastocyst's inner cell mass. Single-cell gene-expression analysis showed that the loss of *NANOG* diverted cells so that they formed cells belonging to layers in the blastocyst called the primitive endoderm and trophectoderm. There was less expression of genes that are characteristic of the epiblast — the cell layer in a blastocyst that gives rise to the embryo (Fig. 1a). The persistence of primitive endoderm cells in human embryos lacking *NANOG* is in contrast to the loss of these cells in mouse embryos with mutant *Nanog*[9–11]. These findings suggest that *NANOG* is essential for